













```

Db      8  NFADELMGISAAISKTAVTUTLEPVKMLIQTPQPSIDFKSQQVVERYSOI INCPREVSKH 67
Q7      65  GOVLESTWESCHLANNVFEYETQALNEATTPWQGLTFVWPHHLEWEYIASHRLASQAA 124
Db      66  QVAVQWCHVANVIEYETLAERAEKAEKHEF  FVDCRHDPSKTCVNIJSCATAC 126
Q7      125  APLGCTVVYELDFARTLAADWKSSTEREERFGLHETLVKITESSGIPGUYGSPSVSVGHI 184
Db      127  AIGLLIVYTHINAFTHLASHQCF  CKKQFTLFLCLAKIYKUTGLLSLYSGPGVSVTGI 185
Q7      185  IIRAAATGVYETAKOMI  FEFKNEHIVVSWHINAGIVIAVAVSVSTPDLIVFRRMMQSC 243
Db      186  IVYKSYGLYDSAKALLFTNKKNTINVLKWAVAQSVTILAGLISYPTTIVERRMMMSG 245
Q7      244  LKG  ADGMYTGVVTCWKEFEDEGTAFFPAGAWSNVLKMGKAGPVLVYNGELKKVI 298
Db      245  FETVETLVYPTTCTWFLAENEDF  JEFFJAWAV  KAGAGAAVGVILLEGLLI 301

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Search completed: January 2 2003, 14:47:32  
 Job time : 19 secs





Fri Jan 3 10:31:14 2003

075746 homo sapien  
P16261 rattus norv  
Q21153 caenorhabdi  
C92258 homo sapien  
P16260 mus musculu  
Q92262 mus musculu  
Q13805 schizosacch  
Q94150 homo sapien  
Q94151 homo sapien  
Q94152 homo sapien  
P55916 homo sapien  
Q94153 mus musculu

34 395 19.1 678 1 CMC1\_HUMAN  
35 285.5 18.8 322 1 GDC\_RAT  
36 287.5 18.6 762 1 CMC1\_CAEFL  
37 396 18.5 325 1 HCP5\_HUMAN  
38 284 18.5 332 1 GDC\_HUMAN  
39 39 284 18.4 325 1 UCP5\_MOUSE  
40 282.5 18.3 326 1 YEN8\_SCHPO  
41 280 18.1 675 1 CMC2\_HUMAN  
42 272 17.6 315 1 MPT\_HUMAN  
43 276 17.5 315 1 SAT8\_HUMAN  
44 265 17.2 312 1 UCP3\_HUMAN  
45 265 17.2 676 1 CMC2\_MOUSE

ADT3\_HUMAN  
ID ADT3\_HUMAN STANDARD: PRT: 298 AA.  
AC P12236: 096049;  
DI 01-06-1989 (Rel. 12, Last sequence update)  
DT 01-NOV-1990 (Rel. 16, Last annotation update)  
UI 15 JUN 2002 (Rel. 41, Last isoform update)  
DE ADP/ATP carrier protein, liver isoform 12 (ADP/ATP translocase 3)  
DE (Adenine nucleotide translocator 3) (ANT 3).  
GN SLC25A6 OR ANT3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RF MEDLINE:8949636; PubMed:2541251;  
RA Coziers A.L., Runswick M.J., Walker J.E.;  
FA "DNA sequences of two expressed nuclear genes for human mitochondrial  
ADP/ATP translocase.";  
RT J. Mol. Biol. 206:261-280(1989).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,  
Margolin J.F.;  
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RJ [3]  
RP SEQUENCE FROM N.A.  
R2 TISSUE=Brain, Cervix, Eye, and Lung;  
RA Staudtera R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases  
[4]  
RN SEQUENCE OF 36 298 FROM N.A.  
RP TISSUE=Liver;  
RA Medline 85121845; PubMed 254183;  
FA Houldsworth J., Attardi G.;  
ET "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
level in adult human liver.";  
EL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
MITOCHONDRIAL INNER MEMBRANE  
CC -1- SUBUNIT: HOMO-DIMER  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
inner membrane  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
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or send an email to [license@isb.sib.ch](mailto:license@isb.sib.ch)).  
EMBL, J03592: AAA36750.1;

ALIGNMENTS

RESULT 1  
ADT3\_HUMAN  
ID ADT3\_HUMAN STANDARD: PRT: 298 AA.  
AC P12236: 096049;  
DI 01-06-1989 (Rel. 12, Last sequence update)  
DT 01-NOV-1990 (Rel. 16, Last annotation update)  
UI 15 JUN 2002 (Rel. 41, Last isoform update)  
DE ADP/ATP carrier protein, liver isoform 12 (ADP/ATP translocase 3)  
DE (Adenine nucleotide translocator 3) (ANT 3).  
GN SLC25A6 OR ANT3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
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RF MEDLINE:8949636; PubMed:2541251;  
RA Coziers A.L., Runswick M.J., Walker J.E.;  
FA "DNA sequences of two expressed nuclear genes for human mitochondrial  
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RT J. Mol. Biol. 206:261-280(1989).  
RL [2]  
RN SEQUENCE FROM N.A.  
RP Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,  
Margolin J.F.;  
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RJ [3]  
RP SEQUENCE FROM N.A.  
R2 TISSUE=Brain, Cervix, Eye, and Lung;  
RA Staudtera R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases  
[4]  
RN SEQUENCE OF 36 298 FROM N.A.  
RP TISSUE=Liver;  
RA Medline 85121845; PubMed 254183;  
FA Houldsworth J., Attardi G.;  
ET "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
level in adult human liver.";  
EL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
MITOCHONDRIAL INNER MEMBRANE  
CC -1- SUBUNIT: HOMO-DIMER  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
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or send an email to [license@isb.sib.ch](mailto:license@isb.sib.ch)).  
EMBL, J03592: AAA36750.1;

US-09-185-904A-33  
Perfect score: 1543  
Sequence: 1 MTEQATISFAKDETAAGTAA...LRMGAFVLVLYDELKKVI 298  
Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5  
Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892  
Minimum DB seq length: 6  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	ADT3_HUMAN	P12236 homo sapien
2	1512	98.0	298	ADT3_BOVIN	P42097 bos taurus
3	1453	94.8	298	ADT2_HUMAN	P05141 homo sapien
4	1451	94.0	298	ADT2_RAT	Q09013 rattus norv
5	1445	93.6	298	ADT2_MOUSE	P51881 mus musculu
6	1424	92.3	298	ADT1_RAT	Q04962 rattus norv
7	1418	91.9	298	ADT1_MOUSE	P44962 mus musculu
8	1417	91.8	297	ADT1_BOVIN	P12235 bos taurus
9	1409	91.3	298	ADT1_HUMAN	Q26365 drosophila
10	1217.5	78.9	297	ADT1_DROME	Q12444 anopheles g
11	1204	79.0	301	ADT1_AROJA	P16692 anopheles g
12	778.5	50.5	307	ADT3_YEAST	P18238 saccharomyc
13	772	50.0	308	ADT1_YEAST	P27080 chlamydomon
14	765	49.8	322	ADT1_CHLRE	Q09188 schizosacch
15	768	49.8	386	ADT1_SCHPO	C22342 gossypium b
16	768	49.8	313	ADT1_GOSU1	P92723 neurexina
17	766	49.6	313	ADT1_NEUR1	P19382 kluyveromye
18	752.5	49.4	355	ADT1_KLUF	P18239 saccharomyc
19	750.5	49.3	318	ADT2_YEAST	P40941 arabidopsis
20	750.5	48.6	385	ADT2_ARATH	P04709 oca mayz (m
21	750.5	48.6	387	ADT1_MAIZE	P25083 solanum tub
22	747	48.5	386	ADT1_SOLEU	P31691 cryza sativ
23	747	48.4	392	ADT1_ORYSA	P12857 oca mayz (u
24	743	48.2	387	ADT2_MAIZE	P31767 arabidopsis
25	742.5	49.1	381	ADT1_ARATH	Q41629 lithium ac
26	740	48.0	331	ADT1_WHEAT	P27081 solanum tub
27	739.5	47.9	386	ADT2_SCHPO	P04710 saccharomyc
28	737.5	47.8	309	ADT1_YEAST	Q41630 triticeum ae
29	727	47.1	331	ADT2_WHEAT	Q26739 caenorhabdi
30	702	19.6	588	CMC2_CAEFL	Q01888 bos taurus
31	300	19.4	430	GDC_BOVIN	G99297 saccharomyc
32	289	19.4	307	CMC2_YEAST	Q19529 caenorhabdi
33	297	19.2	587	CMC3_CAEFL	

Summary: 112892 seqs, 41476328 residues  
Minimum DB seq length: 6  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

Summary: 112892 seqs, 41476328 residues  
Minimum DB seq length: 6  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database: SwissProt\_40.\*

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Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
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Maximum DB seq length: 200000000  
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Minimum DB seq length: 6  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database: SwissProt\_40.\*

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Minimum DB seq length: 6  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
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Maximum DB seq length: 200000000  
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Minimum DB seq length: 6  
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Minimum DB seq length: 6  
Maximum DB seq length: 200000000  
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Maximum Match 100%  
Listing first 45 summaries  
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Minimum DB seq length: 6  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database: SwissProt\_40.\*

Summary: 112892 seqs, 41476328 residues  
Minimum DB seq length: 6  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database: SwissProt\_40.\*



Fri Jan 3 10:31:14 2003

ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)  
 (Adenine nucleotide translocator 2) (ANT 2).  
 G1225A5; Cf ANT2.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID: 9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 KA Molecular Weight: 27,527; ID# J01692P2  
 RA Ku D.-H., Kadan J., Chen S.-T., Chang C.-D., Baserga W., Wurzel J.;  
 RT "The human fibroblast adenine nucleotide translocator gene. Molecular  
 cloning and sequence."  
 RL J. Biol. Chem. 262:4355-4358(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 97166056; PubMed=4041073;  
 RA Battini R., Ferrari S., Kozmarek L., Calabretta B., Chen S.T.,  
 RA Baserga W.;  
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is  
 K1 greatly regulated."  
 RL J. Biol. Chem. 262:4355-4358(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 KA Chen C.-H., Gu Y., Burkaya P., Sirano A., Nigam A.P.,  
 RA Mazzarella R.A., Schlessinger D., Chen E.Y.-X;  
 RL Submitted (unpub) to the EMBL/GenBank/DDBJ databases  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 KA Becker M., Graves T., Oseroff P.;  
 RL Submitted (unpub) to the EMBL/GenBank/DDBJ databases  
 RN [5]  
 RP SEQUENCE OF 47 298 FROM N.A.  
 RC TISSUE=Liver;  
 KA MEDLINE 9412445; PubMed=7620184;  
 RA Houldsworth J., Attardi G.;  
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
 level in adult human liver."  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
 CC -1- DOMAIN: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
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 CC  
 CC EMBL: M7121; AAA51977.1;  
 CC EMBL: J02683; AAA35579.1;  
 CC EMBL: L78810; AAH39246.1;  
 CC EMBL: AC004000; AAB36749.1;  
 CC EMBL: J63591; AAA36749.1;  
 CC DR A25132; A29132;  
 CC PIR: C25116; C28116;  
 CC GeneID: 828109; S 62655  
 CC MIM: 300150;  
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 CC Pfam: PF00153; mito\_carrier\_3;  
 CC PRINTS: PR00926; MITCARRIER  
 CC PROSITE: PS00215; MITOCH\_CARRIER\_3;  
 CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family. 29 1 (POTENTIAL).  
 FT TRANSMEM 12

FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
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 FT CONFLICT 66 G -> E (IN REF. 2).  
 FT CONFLICT 111 R -> L (IN REF. 4 AND 5).  
 FT CONFLICT 162 V -> S (IN REF. 5).  
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 Query Match 94.8% Score 1463; DB 1; Length 298;  
 Rest Local Similarity 92.4%; Pos. No. 6,92,123;  
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 MTEQAFSEAFDFLAGGIAAISKTAAPVIERVKLLQVQIASKQIAADKYKG VDCIVR 60  
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 QY 51 LKFFGVLSIWRGNLANVIRYPTQANPAFKDKYKQIFLGSGYDKKHDFWRYFAGNLSG 120  
 DB 51 LKFFGVLSIWRGNLANVIRYPTQANPAFKDKYKQIFLGSGYDKKHDFWRYFAGNLSG 120  
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 DB 121 GAAGATSLSEVYVILDFAPTEFLAAVSKSTERTETRLGDCIVLHKNSGIRGLCOFSSV 180  
 QY 181 VQGIITVRAAYFGVYDTAKGMLDPPKNTHTIIVSWNIAGTIVTAVAGVSYYPEDTVRRMM 240  
 DB 181 VQGIITVRAAYFGVYDTAKGMLDPPKNTHTIIVSWNIAGTIVTAVAGVSYYPEDTVRRMM 240  
 QY 241 QSGKKGADIVYTGVCWPKTPPDEFCAPFKGANSVLRKMGCAEVLVLYDELRK 296  
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 AC Q09673;  
 DT 01 FEB 1995 (rel. 31, Created)  
 DT 01 FEB 1995 (rel. 31, Last sequence update)  
 DT 16 OCT 2001 (rel. 40, Last annotation update)  
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)  
 DE (Adenine nucleotide translocator 2) (ANT 2).  
 DE SLC25A5 OR ANT2.  
 DE Rattus norvegicus (Rat).  
 DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 DE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 DE NCBI\_TaxID: 10116.  
 DE [1]  
 DE SEQUENCE FROM N.A.  
 DE TISSUE=Liver;  
 DE MEDLINE 94002151; PubMed=8499300;  
 DE Shiohara Y., Yamada M., Yamazaki N., Terada H.;  
 DE "Isolation and characterization of cDNA clones and a genomic clone  
 DE encoding rat mitochondrial adenine nucleotide translocator.";  
 DE Biochim. Biophys. Acta 1152:192-196(1993).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND  
 CC SKELETAL MUSCLE.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 CC  
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 CC  
 CC EMBL: M7121; AAA51977.1;  
 CC EMBL: J02683; AAA35579.1;  
 CC EMBL: L78810; AAH39246.1;  
 CC EMBL: AC004000; AAB36749.1;  
 CC EMBL: J63591; AAA36749.1;  
 CC DR A25132; A29132;  
 CC PIR: C25116; C28116;  
 CC GeneID: 828109; S 62655  
 CC MIM: 300150;  
 CC InterPro: IPR000067; Mit\_carrier  
 CC InterPro: IPR001993; Mitoch carrier  
 CC Pfam: PF00153; mito\_carrier\_3;  
 CC PRINTS: PR00926; MITCARRIER  
 CC PROSITE: PS00215; MITOCH\_CARRIER\_3;  
 CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family. 29 1 (POTENTIAL).  
 FT TRANSMEM 12













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||||| 181 VSVQGLIIYKAAFGCFDTAKGMLPDKNTSIFVSWATACVVTATSCIIISYPLTVPRRM 240
Q7 233 MMQSGERKALINTSTVDCRPVIFPEGCKAFKFAKSNVLCFMCFAFVLYVIFLKKVT 298
||||| 241 MMQSWPCKSEVMYKNTLDGWKRGKQEGSCAFKGAFAFNVLCSTGGALVLYVFEVKALL 300

RESULT 12
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1J ADT_CHLKE STANDARD; PKT: 339 AA.
AC B31632; 1993 (Rel. 2b, Created)
DI 01-JUL-1993 (Rel. 2b, Last sequence update)
DI 01-JUL-1993 (Rel. 36, Last annotation update)
DE ADP.ATP carrier protein (ADP/ATP translocase) (Adenine nuc. eotide
DE translocator) (ANT).
OS Chlorella kessleri.
OC Eukaryota, Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
CX NCBI_taxid=3074;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92084708; PubMed=1748667;
RA Hilgarth C., Sauer N., Tanner W.;
FT "Glucose increases the expression of the ATP/ADP translocator and the
FT glyceralddehyde-1-phosphate dehydrogenase genes in Chlorella.";
FL 3. Biol. Chem. 266:2404-2407(1991).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announc/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: M76669; AAA33027.1;
CC PIR: A41677; A41677.
CC InterPro: IPR002067; Mit_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mito_carr; 3.
CC PRINTS: PS00226; MITOCARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 3.
CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
CC TRANSMEM 14 31 93 2 (POTENTIAL).
CC TRANSMEM 119 136 2 (POTENTIAL).
CC TRANSMEM 178 197 4 (POTENTIAL).
CC TRANSMEM 216 233 5 (POTENTIAL).
CC TRANSMEM 275 299 5 (POTENTIAL).
CC SEQUENCE 361 AA; 32853 MW; 400941769PDA08B CRC64.

Query Match 78.08; Score 1204; DB 1; Length 301;
Best Local Similarity 77.78; Pred. No. 7.5e-100;
Matches 233; Conservative 23; Mismatches 42; Indels 1; Gaps 1;

Q7 1 PF02A 1STADPFLACQIARAIKSTAVAPFVPLDQVHASKQIAADKQYGLVDCI 58
||||| 1 MKKAPVGGAKDIFLAGVLAAYKSTAVAPFVPLDQVHASKQIAADKQYGLVDCI 60
Q7 63 43PFQGVQVFWERNIAWVYPTPTQALNFAFKIKYQVIFGSEVYKHTQVTKWFAAGNA 116
||||| 61 VRIKEDQGIQAWRGLANVYVYPTQALNFAFKIKYQVIFGSEVYKHTQVTKWFAAGNA 120
Q7 119 SGCAGAGLSAGVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 178
||||| 121 SGCAGAGLSAGVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 180
Q7 179 VSVQGLIIYKAAFGCFDTAKGMLPDKNTSIFVSWATACVVTATSCIIISYPLTVPRRM 238

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RESULT 11
ADT_ANOCA
1J ADT_ANOCA STANDARD; PRT: 301 AA.
AC Q27238;
DI 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DI 01-NOV-1997 (Rel. 35, Last annotation update)
DE ADP.ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
DE translocator) (ANT).
OS Anopheles gambiae (African malaria mosquito)
OC Eukaryota, Metazoa, Arthropoda, Insecta; Pancrustacea, Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Culicoidae; Anophelinae.
CX NCBI_taxid=7145;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=93;
RX MEDLINE=94348635; PubMed=8069414;
RA Beard C.B., Crews-Owen A.E., Kumar V.K., Collins F.H.;
RI "A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles
RI gambiae.";
FL 1. Insect Mol. Biol. 3:35-40(1994).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY)
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announc/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: L11618; AAR04104.1;
CC EMBL: L11617; AAR04105.1;
CC InterPro: IPR002067; Mit_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mito_carr; 3.
CC PRINTS: PS00226; MITOCARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 3.
CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
CC TRANSMEM 14 31 93 2 (POTENTIAL).
CC TRANSMEM 175 93 2 (POTENTIAL).
CC TRANSMEM 119 136 2 (POTENTIAL).
CC TRANSMEM 178 197 4 (POTENTIAL).
CC TRANSMEM 216 233 5 (POTENTIAL).
CC TRANSMEM 275 299 5 (POTENTIAL).
CC SEQUENCE 361 AA; 32853 MW; 400941769PDA08B CRC64.

Query Match 78.08; Score 1204; DB 1; Length 301;
Best Local Similarity 77.78; Pred. No. 7.5e-100;
Matches 233; Conservative 23; Mismatches 42; Indels 1; Gaps 1;

Q7 1 PF02A 1STADPFLACQIARAIKSTAVAPFVPLDQVHASKQIAADKQYGLVDCI 58
||||| 1 MKKAPVGGAKDIFLAGVLAAYKSTAVAPFVPLDQVHASKQIAADKQYGLVDCI 60
Q7 63 43PFQGVQVFWERNIAWVYPTPTQALNFAFKIKYQVIFGSEVYKHTQVTKWFAAGNA 116
||||| 61 VRIKEDQGIQAWRGLANVYVYPTQALNFAFKIKYQVIFGSEVYKHTQVTKWFAAGNA 120
Q7 119 SGCAGAGLSAGVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 178
||||| 121 SGCAGAGLSAGVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 180
Q7 179 VSVQGLIIYKAAFGCFDTAKGMLPDKNTSIFVSWATACVVTATSCIIISYPLTVPRRM 238

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OM protein - protein search using sw mod.1

Run on: January 01, 2003, 11:15:30, Search time: 18 seconds  
(without alignments)

584,535 million cell updates/sec

Title: us-09-185-904a-33

Perfect score: 1543

Sequence: 1 MTPQATSFAPFLAAGSIAAA (PROMOTIVIN) REF: 758

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262571 seqs, 2942922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DE seq length: 0

Maximum DE seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:

- 1: us-08-061-871-10
- 2: us-08-061-871-10
- 3: us-08-061-871-10
- 4: us-08-061-871-10
- 5: us-08-061-871-10
- 6: us-08-061-871-10

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1412	91.5	298	3	us-08-061-871-10
2	1412	91.5	298	3	us-08-061-871-10
3	281.5	18.4	291	4	us-09-501-558-2
4	280	18.1	447	4	us-09-160-119-4
5	280	18.1	674	4	us-09-160-119-2
6	250.5	16.2	311	3	us-08-775-009-33
7	250.5	16.2	299	1	us-08-518-878-51
8	250.5	16.2	309	2	us-08-518-878-51
9	250.5	16.2	309	2	us-08-807-861A-51
10	250.5	16.2	309	2	us-08-470-861A-51
11	250.5	16.2	309	3	us-09-210-681-51
12	250.5	16.2	309	3	us-08-946-719A-51
13	250.5	16.2	311	3	us-08-775-009-33
14	250.5	16.2	311	3	us-08-775-009-33
15	245	15.9	432	3	us-09-318-199-4
16	245	15.9	432	3	us-09-318-199-4
17	245	15.9	432	3	us-09-503-579-4
18	245	15.9	432	3	us-09-503-579-4
19	244	15.8	408	3	us-08-775-009-33
20	244	15.8	408	3	us-09-318-199-2
21	244	15.8	408	4	us-09-503-579-2
22	244	15.8	408	4	us-09-503-579-2
23	243.5	15.9	432	3	us-09-318-199-4
24	243.5	15.9	432	3	us-09-318-199-4
25	243.5	15.9	432	3	us-09-503-579-4
26	243.5	15.9	432	3	us-09-503-579-4
27	243.5	15.9	432	3	us-09-503-579-4

28	226.5	14.7	303	2	us-08-807-861A-37	Sequence 37, Appl
29	226.5	14.7	303	2	us-08-470-861A-37	Sequence 37, Appl
30	226.5	14.7	303	2	us-08-210-681-37	Sequence 37, Appl
31	226.5	14.7	303	2	us-08-446-719A-37	Sequence 37, Appl
32	222	14.4	293	4	us-08-501-558-4	Sequence 4, Appl
33	221	13.7	306	5	PCT-US84-08799-1	Sequence 1, Appl
34	205.5	13.3	307	2	us-08-807-861A-56	Sequence 56, Appl
35	205.5	13.3	307	2	us-08-210-681-56	Sequence 56, Appl
36	205.5	13.3	307	2	us-08-446-719A-56	Sequence 56, Appl
37	198.5	12.9	351	3	us-08-933-750C-19	Sequence 19, Appl
38	198.5	12.9	351	3	us-08-933-750C-19	Sequence 19, Appl
39	193	12.5	328	4	us-09-234-613-15	Sequence 15, Appl
40	191	12.4	328	4	us-09-068-140A-15	Sequence 15, Appl
41	191	12.4	328	4	us-09-068-140A-15	Sequence 15, Appl
42	191	12.4	328	4	us-09-068-140A-15	Sequence 15, Appl
43	191	12.4	328	4	us-09-068-140A-15	Sequence 15, Appl
44	181	11.7	289	4	us-09-503-579-6	Sequence 6, Appl
45	180.5	11.7	312	4	us-09-068-140A-10	Sequence 10, Appl
					us-09-188-530-142	Sequence 142, App

## ALIGNMENTS

RESULT 1  
US-08-961-871-10  
Sequence 10, Application US/08961871  
Patent No. 6013858  
GENERAL INFORMATION:  
APPLICANT: Wallace, Douglas C.  
APPLICANT: Graham, Brett H.  
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine  
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods  
NUMBER OF SEQUENCES: 11  
REFERENCE SEQUENCE ADDRESSES:  
ADDRESS: Greenlee, Winner and Sullivan, P.C.  
STREET: 5170 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: US  
ZIP: 80303  
COMPUTER REARABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: P-POS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961.871  
FILING DATE: 31-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/040,017  
FILING DATE: 01-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Forth, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/AGENT NUMBER: 7A-66  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-961-871-10

Query Match 91.5%, Score 1412, DB 3, Length 298;  
Best Local Similarity 88.6%, Prod No 2e-151;  
Matches 264, Conservatio 19, Mismatches 15, Indels 0, Gaps 0;

57 1 MTPQATSFAPFLAAGSIAAAISKTAIVAPIEPVKLLIQVHASKQIAADKQYKGIIVDCIVR 60









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; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRAND: single
; TOPOLOGY: unknown
US-08-518-8749-51

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Query Match: 16.9%, Score 276.5, PA 1, Length 369,  
Best Local Similarity: 24.9%, Prod. 15.6, GC 29,  
Matches: 74, Conserved: 19, Missed: 115, 100% 15

[illegible]

RESULT 10  
US-08-807-86 A-51  
Sopranos, S. Application # 07/040404-01  
Patent No. 5853975  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
TREATMENT OF OBESITY  
TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmunds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS/MS-DOS  
SOFTWARE: Patent In Release #1 0, Version #1 30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-08-807-86 A  
FILING DATE: 26 FEB 1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/518,876  
FILING DATE: 23-AUG-1995  
APPLICATION NUMBER: 08 62,476,965  
FILING DATE: 06-JUN-1995  
APPLICATION NUMBER: US 08/514,620  
FILING DATE: 23-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/EXCISE NUMBER: 7253 266  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 853 5711/7254  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 51:

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? SEQUENCE CHARACTERISTICS:
? LENGTH: 309 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: unknown
? US-08-807-861A-51

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Query Match.	16.2%	Score	250.5,	D3	3:	Length	309;
Best Local Similarity	24.0%,	Pred.	No. 4, 9c	20:			
Matches	74	Conservative	58	Misclassification	17%		
				Models	25,	Cats	8,

[illegible]

RESULT 11  
 US-08-470-868A-51  
 SUBJECT: 51. Application US-08470868A  
 Patent No. 5861485  
 GENERAL INFORMATION:  
 APPLICANT: Tartaglia, Louis C.  
 TITLE OF INVENTION: Compositions and Methods for the  
 Treatment of Body Weight Disorders, Including Obesity  
 NUMBER OF SEQUENCES: 56  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie and Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1 0, Version #1 30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US-08/470,868A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE CHECKLIST NUMBER: 7500-8631-659  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 770-3090  
 TELEFAX: (212) 869-8864  
 TELEX: 60441 PENNIE  
 INFORMATION FOR SEQ ID NO: 51:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 209 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 COMPOSITION: unknown  
 US-08-470-868A-51



STRANDNESS: single  
Topology: unknown  
US-08-946-719A-51

Query Match 16.2% Score 250.5; DB 3; Length 309;  
Best Local Similarity 24.34; Pred. No. 4.5e-20;  
Matches 71; Conservative 50; Mismatches 146; Gaps 8

QY 12 FLAAGTAAATKIAVAPTEPKIILOVCHASK---QIAADKQYKGIQIVIPKPGQVI 68  
DB 17 FLGATTAACIADLTFTFDIAVAPQICGSGGIVPRTVSAGYQVGMGTTIMVTEGPR 76  
QY 19 AFWHLAHVLYELLALGAEFTFTPTGVVFTQFWTEFACHASSGAGATSE 128  
DB 77 SLVAGVAGGKQWASLASEVLELTSVQKQTKS SIHAS TSSSLASTSGALAV 131  
QY 129 GVVVLELFAKFLAALVCKSTETEEFPGICMIVVFTSPSTPGIYQGPSVSVOGIIYF 188  
DB 132 AVAGGILLVAVVFLAALAPAGGGLTSYSLVAGVPIIAGLEDFRHWETSLIVAPRAVW 193  
QY 192 AAYGVVETAT -CHPMPKPTVWVSWPAQWTVAVAGVSVSYHTTVVPPMMGQS 242  
DB 191 GALLVITVLLDALEKALRLLDGCCHISA GATLLIVIAS FVLVVEIYTM 243  
QY 243 GPKCADIWYTVTVQWPKIPDEGGKAFKFGAWSNVIR-GMGGAFVIVLYDELKVI 298  
DB 244 KALGCTSSAGKCALIMLRLGGRPAITELMTEFLGSGWVVMVFTYEGLEKAL 308

RESULT 14  
US-08-775-009-33  
Sequence 33, Application US/08775009  
Patent No. 5935783

GENERAL INFORMATION:  
APPLICANT: Gony, Weillong  
APPLICANT: Emanuel, Beverly S.  
APPLICANT: Budarf, Marcia L.  
APPLICANT: Roe, Bruce  
TITLE OF INVENTION: Rn. 5935783el Genes Mapping in the DiGeorge and  
TITLE OF INVENTION: Velocardiofacial Syndrome Minimal Critical Region  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodstock Health Partners, Inc., Building 5  
ADDRESS: No. 5935783els, LLP  
Street: One Liberty Place 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/775,009  
FILING DATE: 27-DEC-1996

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Trujillo, Doreen Yalko  
REGISTRATION NUMBER: 357719  
REFERENCE/POCKET NUMBER: CH-0661  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-775-009-33

Query Match 16.2% Score 250.5; DB 2; Length 311;  
Best Local Similarity 27.6%; Pred. No. 4.9e-20;  
Matches 84; Conservative 53; Mismatches 135; Gaps 8;

QY 10 PDIAGTAAATKIAVAPTEPKIILOVCHASKIADKQYKGIQIVIPKPGQVLS 69  
DB 20 KALLAGTAAATKIAVAPTEPKIILOVCHASKIADKQYKGIQIVIPKPGQVLS 82  
QY 70 LKAGLAVLKVETFCALREA FFDYFQGLLEGV-KHTQFWFYFACNLAAGCAAGAT 126  
DB 80 LYPALSLVCSIKAAVPECPMFEELSMMFDAQCPLOSP-----PGLGGLGAGVAE 135  
QY 129 SLGVVLELFAPIPIAADVQKSTETPEEPGPHGLPVLKIKSLQGLKGLYKSHSVNGIIL 186  
DB 135 AVVVQPMETVVKVFIHD--QTSNPKTPGFEHCVFTVREGIGKGTVOGLTATVTKGQS 193  
QY 180 YSAAYELVYIASEKMLFUSKHIHIVSWSMIACTIVTAVAGVVEY--FFTVVPPMMGQS 242  
DB 194 NOALPFPVMTSLRWY-QGDNPNKPMNLLITGVGAVAGAAVSFGNTFLDVLKTRMOGLE 252  
QY 243 GPKCADIWYTVTVQWPKIPDEGGKAFKFGAWSNVIR-GMGGAFVIVLYDELKVI 298  
DB 253 AHZ-----YPTLIDGSGVLLKNFGPKAFYKGTVPRLGRVCLDVAIVFYDEWKL 304

RESULT 15  
US-08-937-466-4  
Sequence 4, Application US/08937466  
Patent No. 5846779

GENERAL INFORMATION:  
APPLICANT: Zhang, Ning  
APPLICANT: Amaral, M. Catherine  
APPLICANT: Chen, Jin-Long  
TITLE OF INVENTION: UCP3 Genes  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,466  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/POCKET NUMBER: 197-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-937-466-4

Query Match 15.9% Score 245; DB 3; Length 432;  
Best Local Similarity 26.8%; Pred. No. 3.4e-19;  
Matches 79; Conservative 50; Mismatches 144; Gaps 8;

QY 12 FLAAGTAAATKIAVAPTEPKIILOVCHASKIADKQYKGIQIVIPKPGQVLSFW 71

















? SEQ ID NO: 2  
? LENGTH: 477  
? TYPE: PRT  
? ORGANISM: Homo sapiens  
US-09-777-921A-2

Query Match 23.8%; Score 368; DB 10; Length 477;  
Best Local Similarity 32.7%; Pred. No. 16-29;  
Mismatch 97; Occurrence 60; Mismatch 112; Indels 22; Gaps 10.  
QY 10 KDLASLAAAEKTAIAETEPVKLLGVQVQASFKQAAKQYFGIVGIVTETPEQGVLS 69  
DB 196 RQVLAAGACAGAVSTSTAPDPIKIMQV-HGSK---SDKM-NIFGSEFGMKEGGIPS 249  
QY 70 FWRANLANVIFPEPTAAINFAKPTFTETFLGVTFHIGTWPIFACNLASGAGATSLC 129  
DB 250 LWRNGTNVIRIAPETAVTFWAVEYQVKEELLEEGQKIGTETPEFISGM-----AGATACT 304  
QY 130 EVVGLGFARTAAADAKGKSTETPEFGKIDFTAKTKESDTPRIYQGFVSVDGIIYYRA 189  
DB 305 FLVPMVMKIRLA--VKKIG---QYSGTYDAKKIKHGGIGAPYKGVVFNLLGIIPIYAG 359  
QY 190 AYGVYELAK-----GNLITFENCHIVVSRHLAGTIVAVAGVVSYSYFELIVPEFMMMSGE 244  
DB 460 IDAVVELLSYWLDFNFKDSVMPGVNVLGGALSSDGGFASYPLALVPTPMGACAVL 419  
QY 245 FQADIMYPTIVTWPTETPEFGKATPEKZAHEN---VLEPGMGAFVLVLYDELEKVI 298  
DB 420 EGKQQL--NNVGLPRRTESREGIDCLYRGLTPNFMKVLPAVGISY--VVVENMKQTL 472

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Job time : 15 secs



















